

MARIANO SANTORO¹, PETER CHAERLE², YANNICK LARA¹, BENOIT DURIEU¹, KIM BEETS¹,
OLGA CHEPURNOVA², VÉRONIQUE SIMONS¹, WIM VYVERMAN², ANNICK WILMOTTE¹

¹BCCM/ULC, InBioS - Centre for Protein Engineering, University of Liège, Liège - 4000, Belgium

²BCCM/DCG, Protistology & Aquatic Ecology, University of Gent, Gent - 9000, Belgium

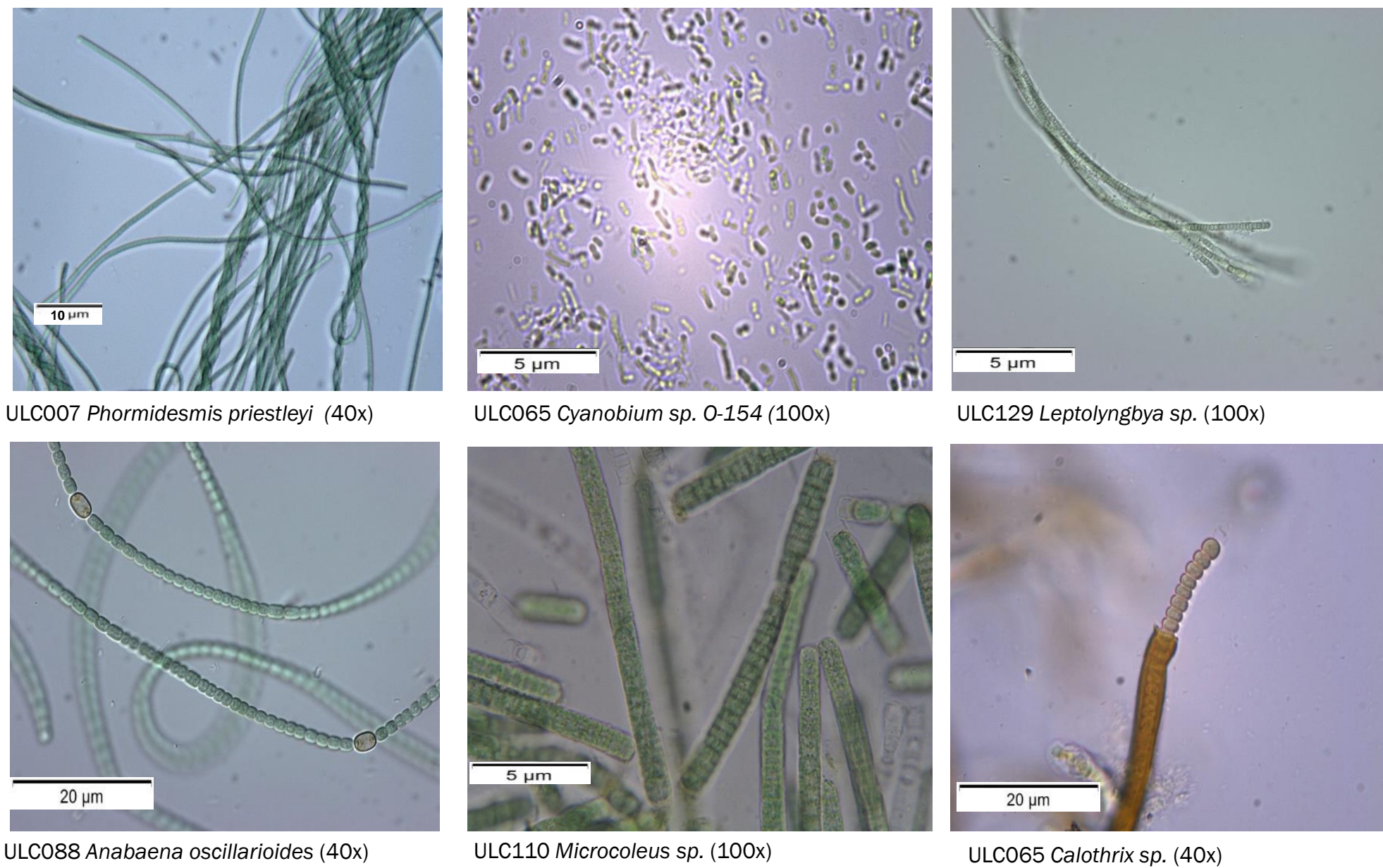
*Correspondence: mariano.santoro@uliege.be

BCCM/ULC

The BCCM/ULC collection has been funded since 2011 by the Belgian Science Policy Office and belongs to the consortium of Belgian Co-Ordinated Collections of Microorganisms. It currently holds **175** cyanobacterial strains (more than 100 of polar origin) belonging to the orders of *Synechococcales*, *Oscillatoriales*, *Pleurocapsales*, *Chroococcidiopsidales* and *Nostocales* (<http://bccm.belspo.be/about-us/bccm-ulc>).

Polar strains as potential sources of novel secondary metabolites

The bioinformatic analysis of the genomes of strains **ULC007**, **ULC065** and **ULC129** (Tab. 1) showed the presence of gene clusters for Non Ribosomal Peptide Synthetases (NRPS), Polyketide Synthases (PKS), hybrid clusters and other types of secondary metabolites (Figs. 2, 3) (Lara & Durieu, unpublished data). The draft genome of the antarctic freshwater strain **ULC007** *Phormidesmis priestleyi* is **the first one** ever determined for an axenic cyanobacterium from Antarctica [1].

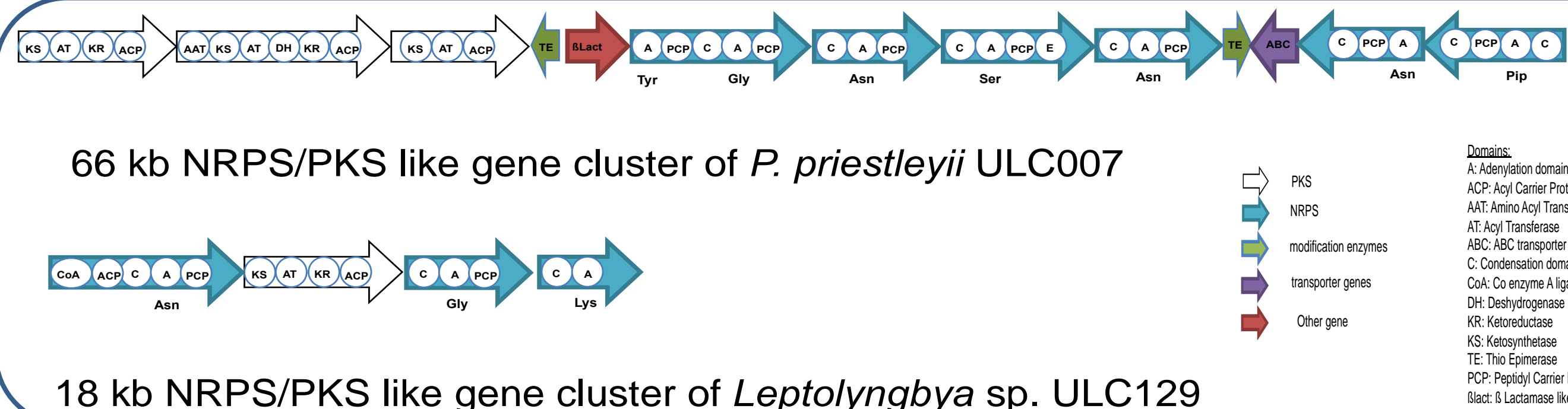


Aim of BCCM/ULC

The ULC public collection serves as one of the largest **Biological Resource Centres** to conserve 'ex situ' and document the biodiversity of **Polar cyanobacteria**, their molecular mechanisms of adaptation to cold stress in Antarctica, as well as their production of potential bioactive compounds which can be used for both biotechnology or biomedical applications. ULC adjusts its policies to guarantee **safe and legally** fit-for-use microbiological material and data for its clients.

| Strain | ULC007 | ULC065 | ULC129 |
|--------------------------------|---------|----------------------|---------|
| Length assembly | 5802032 | 1944012 ₈ | 9402053 |
| Number contigs | 115 | 20290 | 23904 |
| Largest contig | 497161 | 132929 | 77521 |
| Small contigs (<1000 pb) | 107 | 3387 | 3299 |
| GC % | 48.64 | 65.84 | 52.55 |
| N50 | 188801 | 6838 | 5754 |
| L50 | 12 | 303 | 251 |

Tab. 1. Genome sequence assembly results for ULC007 (axenic strain) and ULC065 and ULC129 (two non-axenic strains).

18 kb NRPS/PKS like gene cluster of *Leptolyngbya* sp. ULC129

The strain ULC007 draft genome is 5,684,389 bp long, distributed into 118 contigs, with an average G+C-content of 48.6%, containing 5.604 PEGs, of which 22.2% with no clear homologues in known genomes.

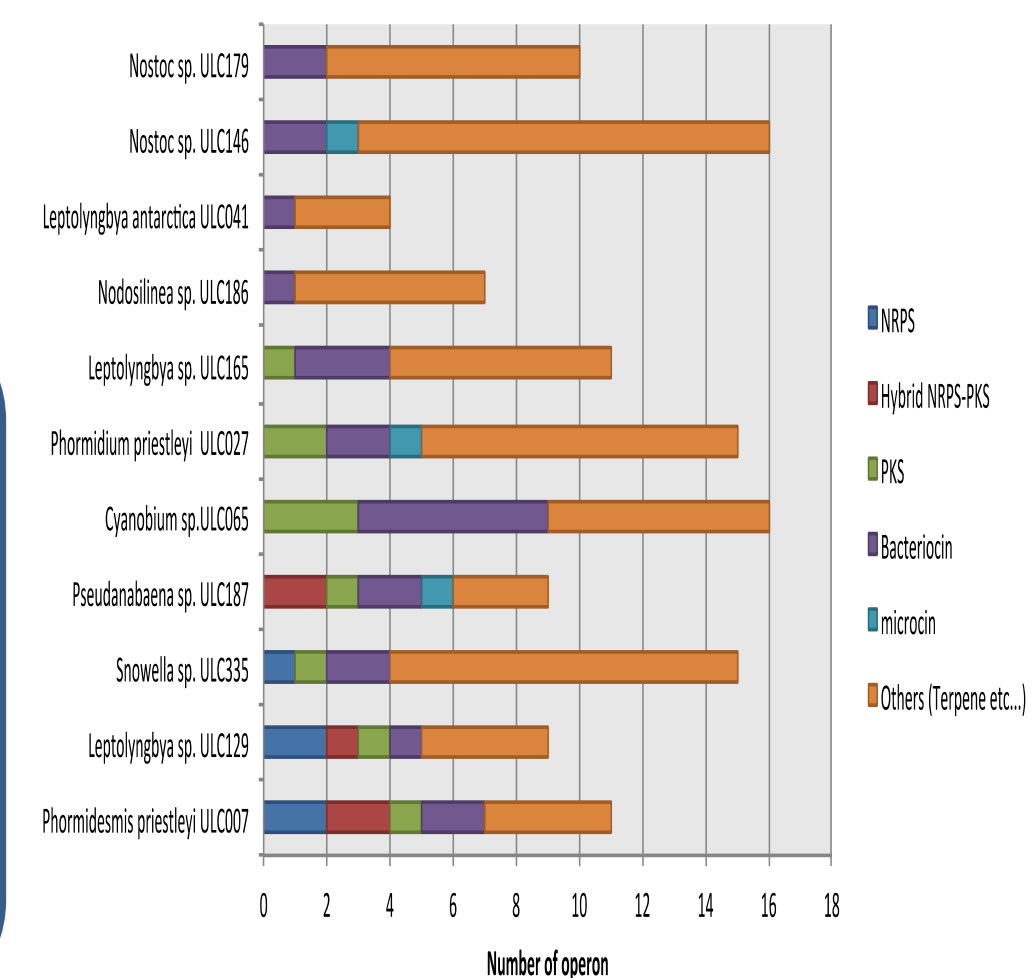
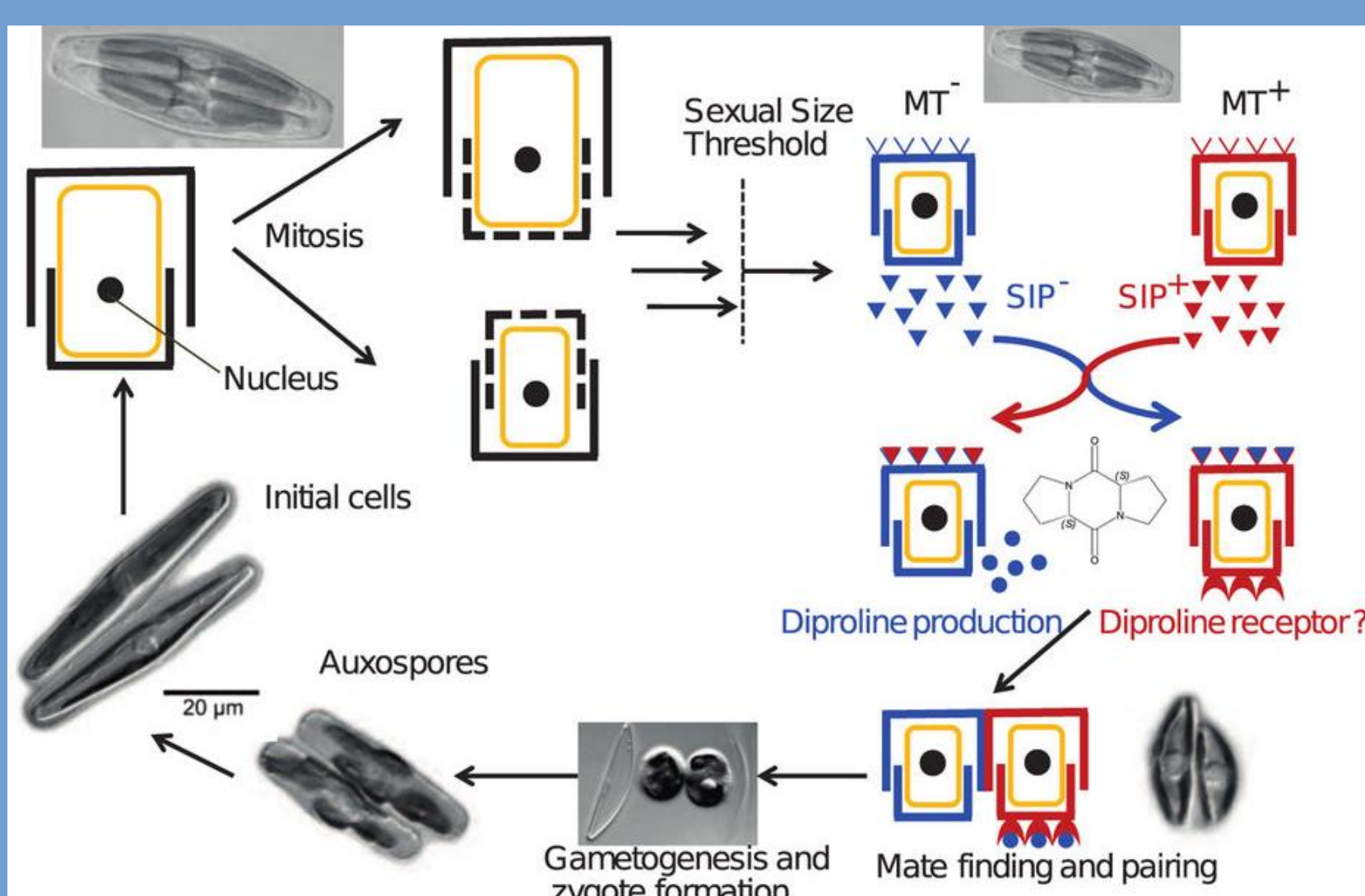


Fig. 3 Strains' content in gene clusters encoding NRPS and PKS – which synthesizes peptides responsible for the production of the secondary metabolites NRPS and PKS – along with other gene clusters involved in the production of secondary metabolites with complex structures and pharmaceutical potential (terpenes, cyanobactins, siderophores, etc).

BCCM/DCG

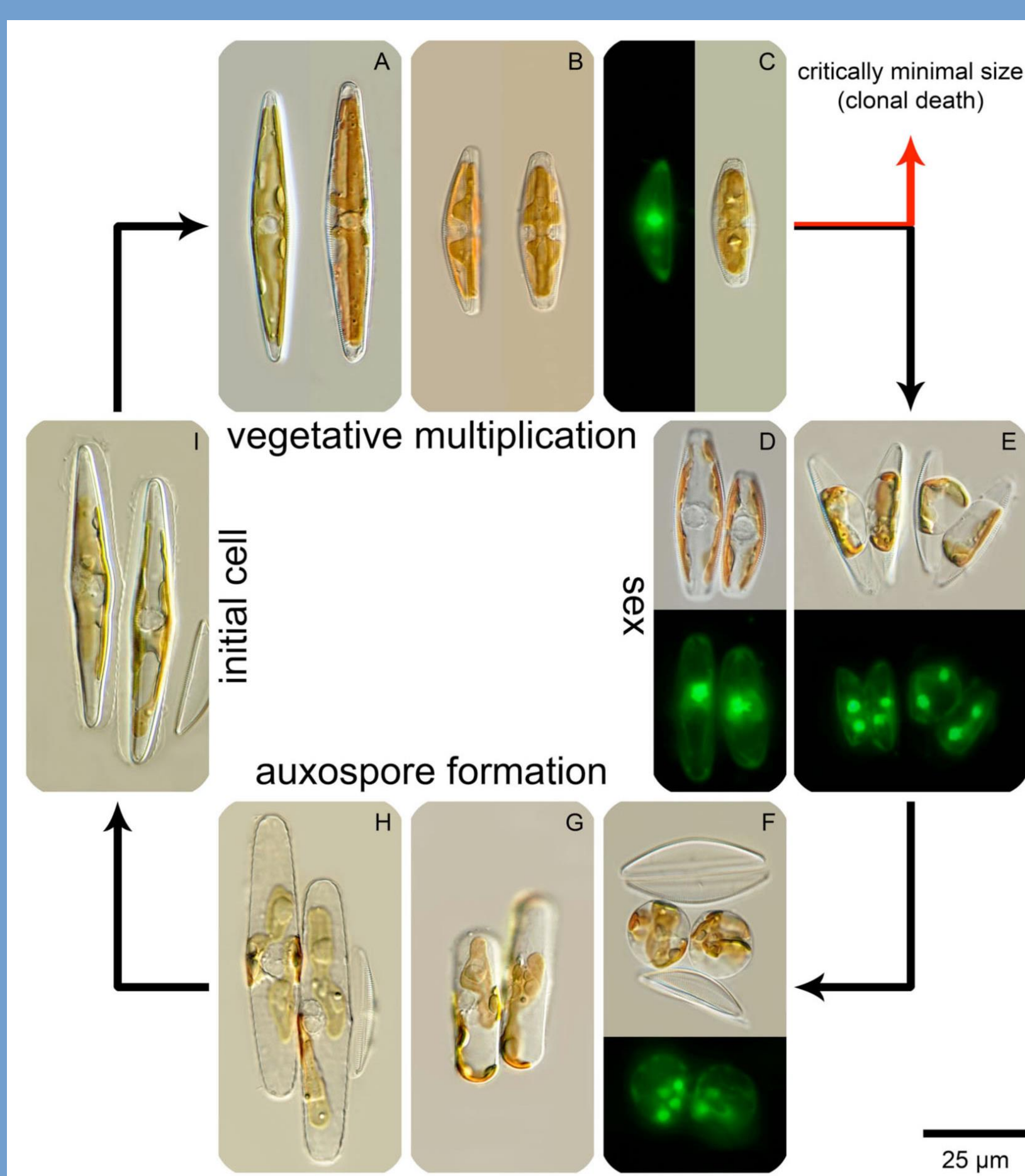
- The BCCM/DCG collection is the only culture collection worldwide specialized in diatoms, the most species rich and ecologically important group of algae. Other microalgae interesting from a scientific or applied perspective are also included in our collection.
- This BRC currently holds 514 publicly available strains (all the isolates are original, from a wide geographic area) belonging to 48 species (representing all the principal phylogenetic lineages and ecological groups) most of which are cryopreserved to limit genetic drift.

Keystone strains



Scheme illustrating the sex-inducing pheromone (SIP+ and SIP-) interaction between MT+ and MT- *Seminavis robusta* cells (DCG0096, DCG0097, DCG0105 and DCG0107). MT- secretes the attraction pheromone diproline which leads to mate finding and pair formation, after this, gametes and zygotes are formed [2].

Our knowledge is your strength



A defining characteristic of all diatoms is their restrictive and bipartite silica cell wall that causes them to progressively shrink during asexual cell division which eventually leads to strain demise. Although asexual auxosporulation occurs in some species, controlling sex in diatoms is not only the key for the maintenance and survival of diatom strains it is also indispensable for breeding and mass culturing [3]. Data on mating system of the strains, auxosporulation type, auxosporulation threshold, initial cell size, and minimal cell size is available in our database.

<http://bccm.belspo.be/about-us/bccm-dcg>

Services

- Worldwide supply of living microalgae strains
- We accept public deposits and safe deposits of microalgae strains
- Identification of microalgae based on morphology and DNA
- Biochemical analysis (pigment analysis, protein assays, etc.)
- Tailor made training and consulting (cryopreservation, culturing algae, etc.)
- Light microscopy and scanning electron microscopy images of algae
- Isolate microalgae, grow and scale up clean microalgae cultures
- Cell imaging combining automated digital microscopy and conventional microplate detection
- State of the art Imaging Flow Cytometry (ImageStream®X)

References

- [1] Lara et al. 2017. Draft genome sequence of the axenic strain *Phormidesmis priestleyi* ULC007, a cyanobacterium isolated from Lake Bruehwiler (Larsemann Hills, Antarctica). Genome Announc 5: e01546-16.
- [2] Moeyes S. et al. 2016. A sex-inducing pheromone triggers cell cycle arrest and mate attraction in the diatom *Seminavis robusta*. Sci Rep 6: 19252.
- [3] Chepurnov, V.A., Chaerle, P., Vanhoutte, K. & Mann D.G. (2012). How to breed diatoms: examination of two species with contrasting reproductive biology. In: R. Gordon and J. Seckbach (eds.) The Science of Algal Fuels. Cellular Origin, Life in Extreme Habitats and Astrobiology Vol. 25. Springer: Dordrecht, XXXIII, 506 p.